

# Mechanisms of haplotype divergence at the RGA08 NBS-LRR locus in wild banana: *Musa balbisiana*

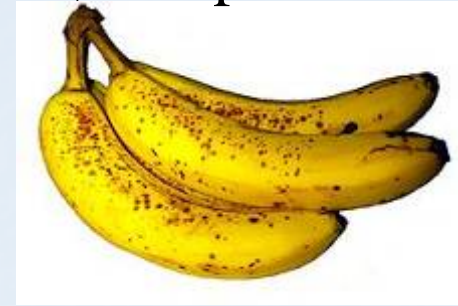
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CIRAD



# Banana is a giant herb

Plant Genomics European Meetings (Plant GEM), 2009/10/07-10, Lisbon, Portugal.

A bunch of fruits, composed of hands and fingers



a pseudo stem formed of tightly packed leaves



Vegetative propagation through suckers



# An important plant with complex genetics

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**Genus**  
*Musa*

*Musa acuminata*

*Musa balbisiana*

**Diploid/triploid**  
**cultivars**



**100 billions of tons production**

**90 billions of tons local consumption**

AA



AAA



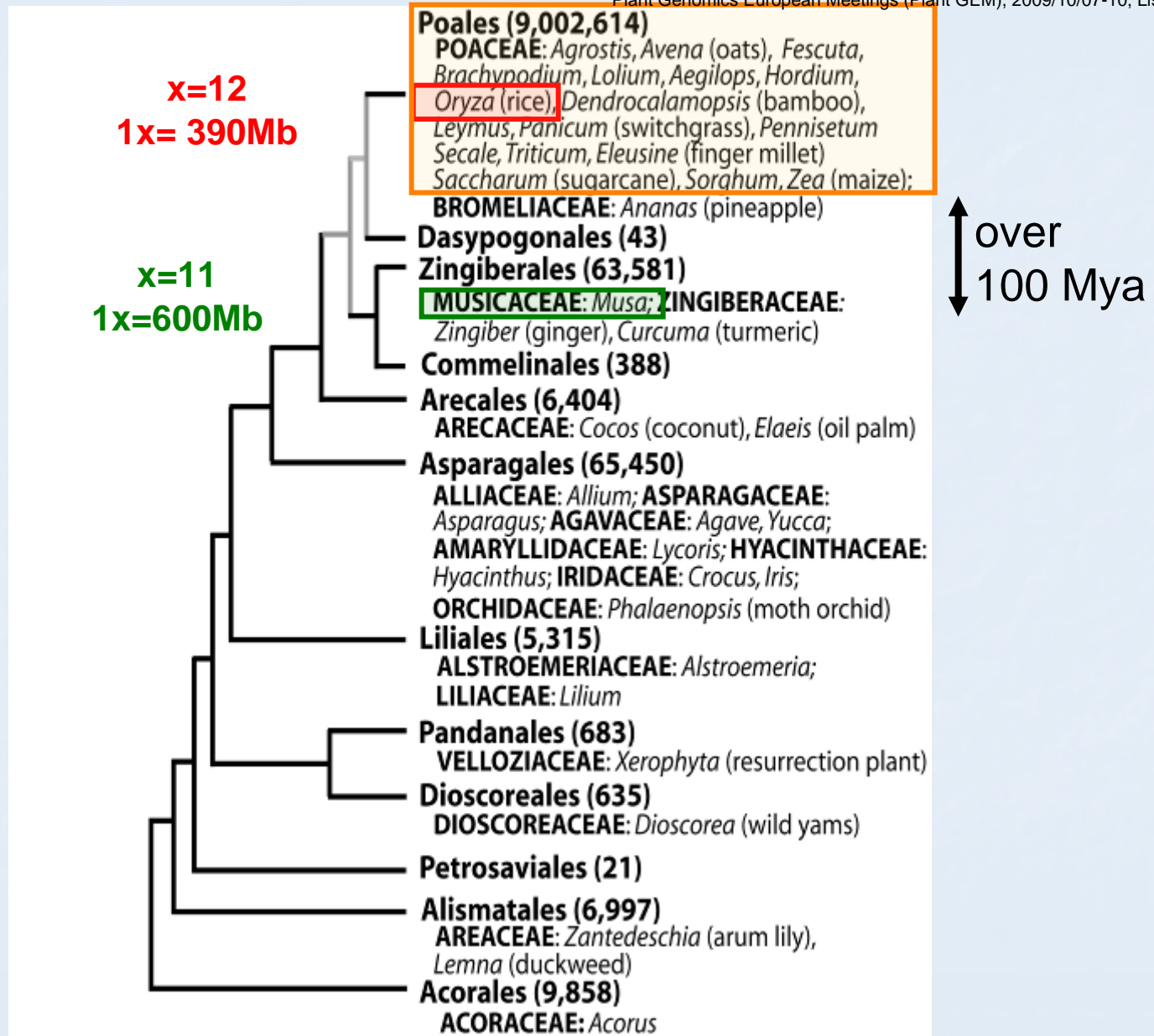
AAB



ABB

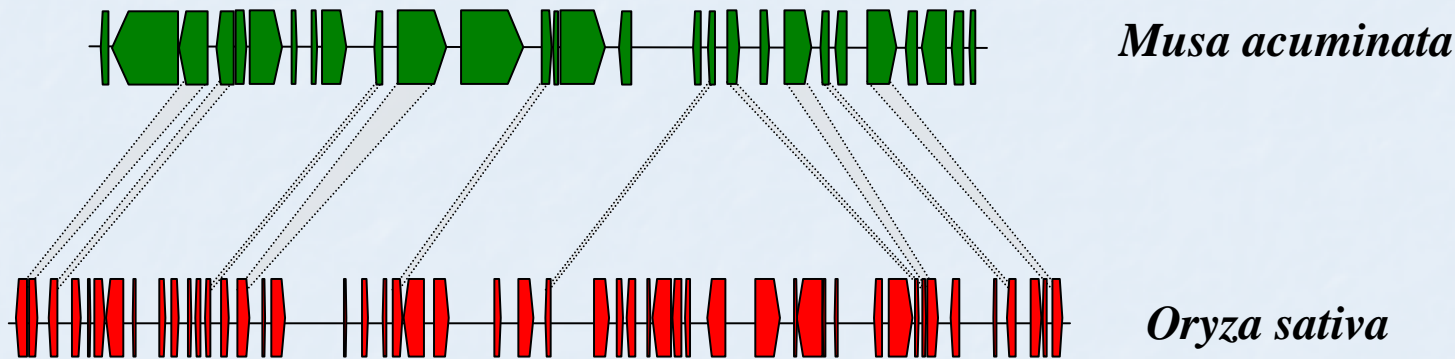
# Bananas belong to a sister group of Poales

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# Comparative genomics of banana

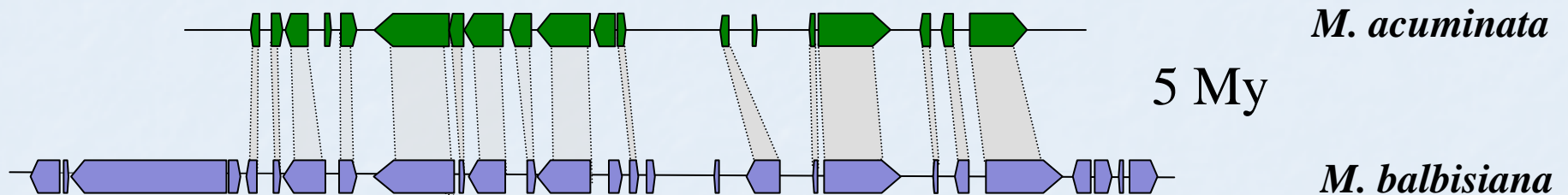
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- 9 out of 17 BAC clones with partial synteny
- traces of synteny retained over 120 million years of divergence

# Comparative genomics within the Musaceae

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- high level of synteny
- intergenic regions are variable

# Musa diversity: the *Musa balbisiana* genome

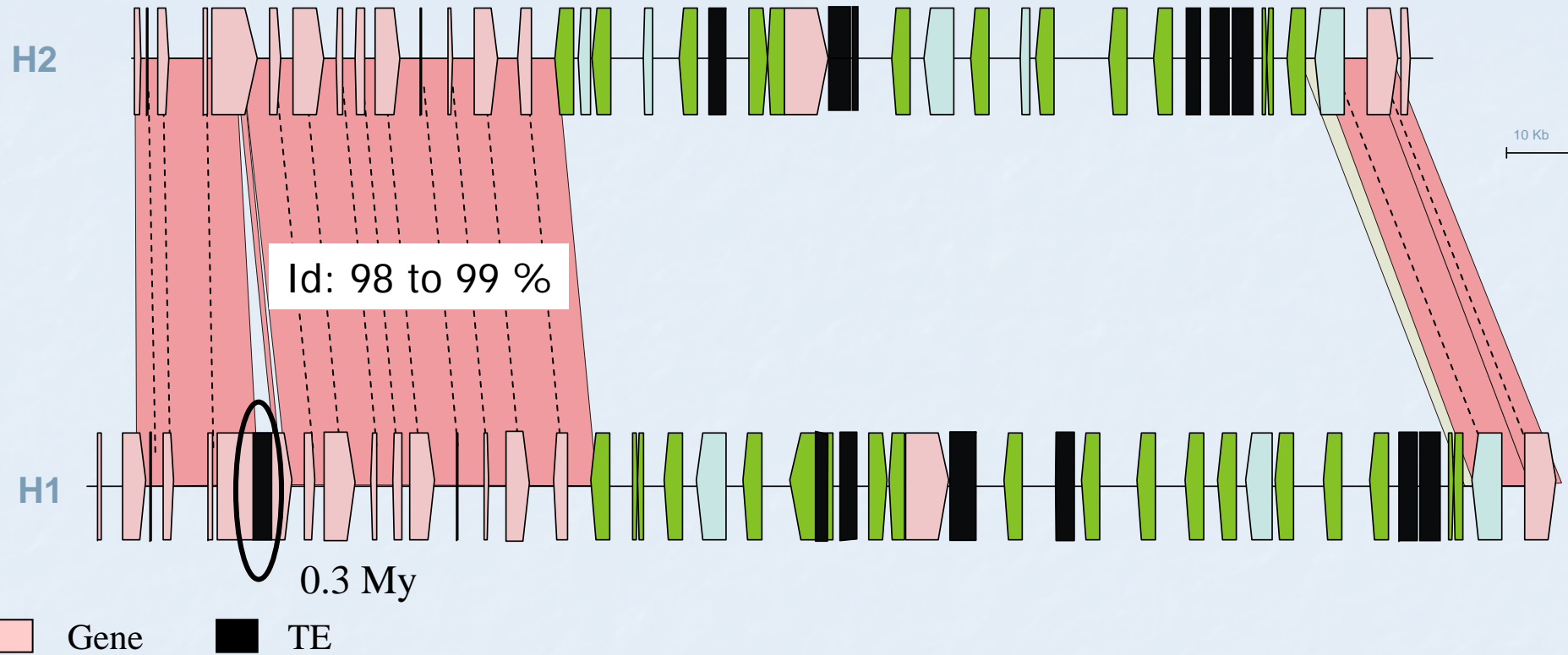
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- *Musa balbisiana*: wild diploid species  $x = 11$
- Involved in the genomic composition of cultivars (plantain)
- High vigor and disease resistance
- Two genomic regions identified and sequenced containing multiple RGAs: 226kb and 252Kb
- Genetic mapping → allelic regions

# Haplotype divergence at the MARGA08 cluster

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- Flanking gene-rich regions (90 kb) are highly conserved
- Haplotype divergence : 1 My (Musa A/B: 4,6 My)
- TEs participate to haplotype divergence (2 indels, 5.3 kb)
- Complex pattern in the RGA cluster, higher TE density



# The MARGA08 gene family

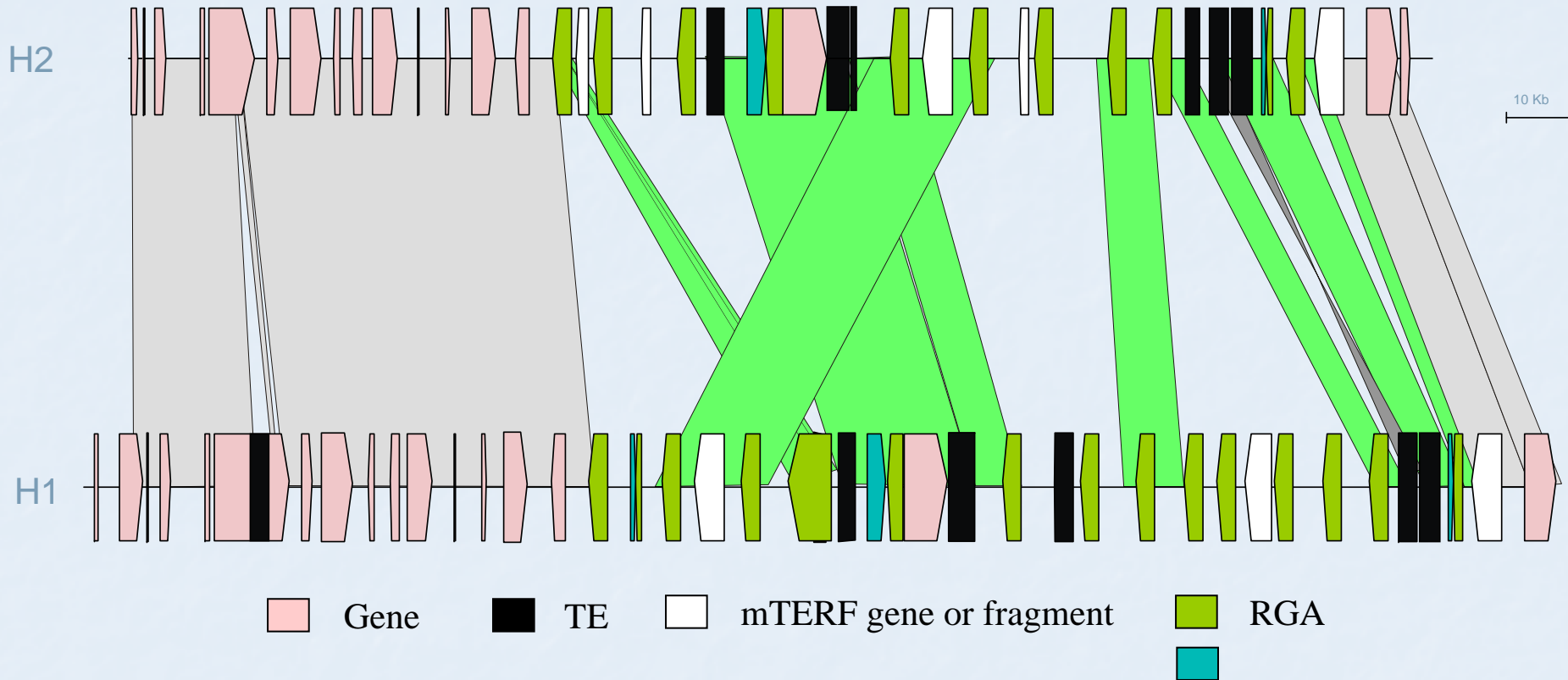
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- 31 NB-LRR genes of the same family (average identity > 80%)
- 2 clades
- 9 Allelic pairs

# Fine genomic structure : alleles and/or paralogs

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- Evolution through tandem and inverted gene duplication, segment duplication, TE activity, diversifying selection
- Differential expansion of the two RGAs clades on the two DNA strands and between haplotypes
- 21 kb size difference between the haplotypes at this locus.

# Conclusion

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- One of the largest single family RGA cluster identified in plants.
- High sequence conservation in gene rich regions of *M. balbisiana*
- Recent TE activity contributes to sequence divergence
- Considerable variation exist between haplotypes of one plant in the repertoire of RGA
- The “MUSATRACT” ANR funded banana genome sequencing project is ongoing (Genoscope, CIRAD and GMGC). Sequencing of the doubled haploid Pahang clone (*M. acuminata*, genome A).

# Acknowledgements

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Thank you for your attention



(Abstracts selected for Oral Presentation in Sessions 1-9 of the 8<sup>th</sup> PlantGEM)

## Session 5 – GENOME STRUCTURE, EVOLUTION AND COMPARATIVE GENOMICS

### GENOME EVOLUTION BY POLYPLOIDIZATION: BACKCROSS ENHANCES DNA SEQUENCE RESTRUCTURING IN TRITICALE

Miguel Bento<sup>1</sup> Augusta Barão<sup>1</sup>; Perry Gustafson<sup>2</sup>; Wanda Viegas<sup>1</sup>; Manuela Silva<sup>1</sup>

<sup>1</sup>CBAA, Instituto Superior de Agronomia, Technical University of Lisbon, Lisboa; <sup>2</sup>Curtis Hall, University of Missouri, Columbia, USA

### CONSTRUCTION OF AN SSR-BASED LINKAGE MAP FOR CYNARA CARDUNCULUS

Ezio Portis<sup>1</sup> Alberto Acquadro<sup>1</sup>; Davide Scaglione<sup>1</sup>; Giovanni Mauromicale<sup>2</sup>; Rosario Mauro<sup>2</sup>; Chris A. Taylor<sup>3</sup>; Steven J. Knapp<sup>3</sup>; Sergio Lanteri<sup>1</sup>

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### SEX-DEPENDENT DIFFERENCES IN TRANSCRIPTION OF TRANSPOSABLE ELEMENTS IN A DIOECIOUS PLANT SPECIES

Tomas Cermak<sup>1</sup> Roman Hobza<sup>1</sup>; Zdenek Kubat<sup>1</sup>; Boris Vyskot<sup>1</sup>; Eduard Kejnovsky<sup>1</sup>

<sup>1</sup>Institute of Biophysics, ASCR, v.v.i.

### MECHANISMS OF HAPLOTYPE DIVERGENCE AT THE RGA08 NBS-LRR LOCUS IN WILD BANANA (MUSA BALBISIANA)

Genome structure, evolution and comparative genomics

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